

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22, Search time 4172.38 seconds

(Without alignment)
11136.303 Million cell updates/sec

Title: US-09-910-428-3

Perfect score: 2869

Sequence: 1 ctcgaagatccctgctgctg.....ataagaagattagagctc 2869

Scoring table: IDENTITY: 100, Gap: 10, Gap: 10

Searched: 16154066 seqs, 400774376 residues

Total number of hits satisfying chosen parameters: 32388132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:
1: em_estdb:
2: em_estdb:
3: em_estdb:
4: em_estdb:
5: em_estdb:
6: em_estdb:
7: em_estdb:
8: em_estdb:
9: em_estdb:
10: em_estdb:
11: em_estdb:
12: em_estdb:
13: em_estdb:
14: em_estdb:
15: em_estdb:
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18: em_estdb:
19: em_estdb:
20: em_estdb:
21: em_estdb:
22: em_estdb:
23: em_estdb:
24: em_estdb:
25: em_estdb:
26: em_estdb:
27: em_estdb:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match length	DB	ID	Description
C	1	506.4	17.7	574	10	AV600094	AV600094
C	2	495.4	17.3	547	10	AV65727	AV65727
C	3	494.2	17.2	548	10	AV65123	AV65123
C	4	461.8	16.1	489	12	BF65399	BF65399
C	5	454	15.8	490	12	HC467318	HC467318
C	6	445.8	15.6	707	10	AV611460	AV611460

C	7	432	15.1	483	10	AM69746	AM69746
C	8	430.8	15.0	447	10	AM484290	AM484290
C	9	424	14.8	542	12	BE69383	BE69383
C	10	422.4	14.7	541	10	BE67659	BE67659
C	11	411.4	14.3	484	13	B1680692	B1680692
C	12	402.4	14.0	745	13	B1184173	B1184173
C	13	398.4	13.9	2703	17	AF101616	AF101616
C	14	394.6	13.8	549	12	AF101616	AF101616
C	15	389.2	13.6	276	11	BE69383	BE69383
C	16	386.2	13.5	864	12	BE69383	BE69383
C	17	380.6	13.3	633	13	B1402610	B1402610
C	18	378.4	13.2	840	12	HC676540	HC676540
C	19	377.6	13.2	493	10	AM426322	AM426322
C	20	377.2	13.1	553	13	BM030689	BM030689
C	21	374.8	13.1	916	14	BM030689	BM030689
C	22	372.6	13.0	1452	11	AK018251	AK018251
C	23	369.6	12.9	4756	17	AO639843	AO639843
C	24	368.8	12.9	441	10	AV665726	AV665726
C	25	367.2	12.8	831	17	BH108484	BH108484
C	26	366.4	12.8	795	17	AC985916	AC985916
C	27	366	12.8	709	17	B76195	B76195
C	28	365.2	12.7	851	14	BM024657	BM024657
C	29	363.8	12.7	537	13	BM024657	BM024657
C	30	363.8	12.7	854	14	BM024657	BM024657
C	31	362.8	12.6	840	12	HC676540	HC676540
C	32	361.6	12.6	792	17	AZ642358	AZ642358
C	33	360.2	12.6	366	10	AM445136	AM445136
C	34	360.2	12.6	829	17	AZ642358	AZ642358
C	35	359	12.5	829	17	AZ642358	AZ642358
C	36	359	12.5	1340	11	HC034939	HC034939
C	37	358.4	12.5	543	10	HE014743	HE014743
C	38	358	12.5	709	17	B16509	B16509
C	39	357.4	12.5	734	17	AZ642358	AZ642358
C	40	357.2	12.5	689	17	AZ642358	AZ642358
C	41	356.4	12.4	893	17	BH089300	BH089300
C	42	356.2	12.4	799	17	AZ642358	AZ642358
C	43	355	12.4	709	17	AZ642358	AZ642358
C	44	354.8	12.4	760	17	AZ642358	AZ642358
C	45	354.8	12.4	838	17	BH083966	BH083966

ALIGNMENTS

RESULT 1
LOCUS: AV600094/c 574 bp mRNA linear EST 27-NOV-2001
DEFINITION: AV600094 Bos taurus cartilage fetus Bos taurus cDNA clone
ACCESSION: E10CA048A02.57, mRNA sequence.
VERSION: AV600094.1 GI:9718839
KEYWORDS: EST.

SOURCE: AV600094.1 GI:9718839

ORGANISM: EST.

REFERENCE: Bos taurus
Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:
Bovidae: Bovinae: Bos.
1 (bases 1 to 574)

AUTHORS: Takasuga A., Hiratsuka S., Tsubota A., Suzuki H., Aso H.

TITLE: Isolation of a high throughput EST sequencing system using

poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs

Nucleic Acids Res. 29 (22), E108 (2001)

Journal MEDLINE

COMMENT: 21570554

Contact: Yoshikazu Sugimoto

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Single pass sequencing.

AV595123		598 bp	mRNA	liver	EST	27-NOV-2001
DEFINITION	AV595123 Bos taurus cartilage fetus Bos taurus cDNA clone					
ACCESSION	E1CAG017601.5, mRNA sequence.					
VERSION	AV595123					
KEYWORDS	AV595123.1 GI:9711673					
SOURCE	EST.					
ORGANISM	Bos taurus					
REFERENCE	Parkayyara; Moryaza; Chervatka; Oranovskaya; Vertebnitsa; Buteleostomi; Mammalia; Ruminantia; Bovidae; Bovinae; Bovinae; Bovidae; Bovidae; Bovinae; Bovinae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Bovidae; Takaue; A., Hirotsune, S., Itoh, R., Jihohzono, A., Suzuki, H., Aso, H. and Sugimoto, Y. Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs					
TITLE	Nucleic Acids Res. 29 (22), E108 (2001)					
JOURNAL	21570554					
MEDLINE	Contact: Yoshikazu Sugimoto					
COMMENT	Animal Genetics Division Shirakawa Institute of Animal Genetics Osakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan Tel.: 81-248-25-5641 Fax: 81-248-25-5725 Email: kazusugi@ccoc.ocn.ne.jp Single pass sequencing. This clone was obtained from a polyA deleted cDNA library.					
FEATURES						
Source	Location/Qualifiers 1..598 Version: "Bos taurus" /db_xref="taxon:9913" /clone="E1CAG017601" /clone_lib="Bos taurus cartilage fetus" /issue_type="cattleage" /dev_stage="fetus" /lab_host="DH10B" /note="Vector: pCDL1; Site_1: SalI; Site_2: NotI; Poly A was deleted from a NotI site"					
HASH COUNT	119 a 123 c 129 g 225 t 2 others					
ORIGIN						
Query Match	17.2%; Score 494.2; DB 10; Length 598;					
Best Local Similarity	94.0%; Pred. No. 2,36-78;					
Matches 545; Conservative	0; Mismatches 30; Indels 5; Gaps 3;					
OY	1466 GGCGCCAGTTTCATGCCCTCATGTAAGACTGTATCAATGATTCTTTAAATGGCGAG	1525				
DB	19 GTGGCGAGTTTCATGCATATATTAATAATGAATGATCTTTAAATGGCTGAG	78				
OY	1566 TAATATCCATGTCGTATATATGACACACCTCTTCAATCCATGACACACACACAC	1585				
DB	79 TAAATCCCATGTCGTATATGACACACCTCTTCAATCCATGACACACACACAC	138				
OY	1586 CTAAGTTTTCATGTCGTATATGACACACCTCTTCAATCCATGACACACACAC	1645				
DB	139 CTAGCTTCCTTCATGTCGTATATGACACACCTCTTCAATCCATGACACACAC	198				
OY	1646 GTGTTTTCCTTCATGTCGTATATGACACACCTCTTCAATCCATGACACAC	1705				
DB	199 GTGTTTTCCTTCATGTCGTATATGACACACCTCTTCAATCCATGACACAC	257				
OY	1706 TAAGCACCTTCATGTCGTATATGACACACCTCTTCAATCCATGACACAC	1765				
DB	258 TATATGATTCATGTCGTATATGACACACCTCTTCAATCCATGACACAC	317				
OY	1766 ACTAGTTTCATGTCGTATATGACACACCTCTTCAATCCATGACACAC	1825				
DB	318 ACTAGTTTCATGTCGTATATGACACACCTCTTCAATCCATGACACAC	377				
OY	1826 CATTTATATTTGACACCTCTTCAATCCATGACACACCTCTTCAATCCAT	1885				

[illegible]

RESULT 8

AM484290/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

MEDLINE

FEATURES

SOURCE

LOCALIZATION

FEATURES

SOURCE

LOCALIZATION

FEATURES

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FEATURES

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LOCALIZATION

FEATURES

SOURCE

LOCALIZATION

FEATURES

SOURCE

RESULT 9

BE99983/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

MEDLINE

FEATURES

SOURCE

LOCALIZATION

FEATURES

SOURCE

LOCALIZATION

FEATURES

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[illegible]

RESULT 10	
HE667659	
LOCUS	HE667659
DEFINITION	541 bp mRNA linear EST 25-APR-2001
ACCESSION	1554433 MARC 480V Bos laurus cDNA 5', mRNA sequence.
VERSION	BE667659
KEYWORDS	BE667659.1 GI:10028250
SOURCE	EST.
COW.	

ORGANISM	REFERENCE
Pos. faunas	
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;	
Bovidae; Bovinae; Bos.	
1 (Bos 1 to 541)	
Smith, T. P. L., Grosse, W. M., Fraking, B. A., Roberts, A. J., Stone, R. T.,	
AUTHORS	

TITLE	Sequence evaluation of four pooled cDNA libraries and construction of a gene index for cattle
JOURNAL	Genome Res 11 (4), 626-630 (2001)
COMMENT	
MEDLINE	21180013
CONTACT	Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mismatch 1
and -mismatch 12 options.
PCR Primers
FORWARD: AGCAACACCTATGACCAAT
BACKWARD: GTTTTCCTATCAGAGC
Plate: 66 row: D column: 24
Seq primer: ATTACCTACCACTATAC

```
FEATURES
SOURCE
LOCATION/QUANTITIES
1. .541
/organism-"Hos taurus"
/db_xref-"taxon:9913"
/clone_11b-"MARC 4B0V"
```

BASE COUNT	ORIGIN
99 a	97 c 110 g 235 t

Query Match	14.78;	Score 422.4;	DB 10;	Length 541;
Best Local Similarity	94.38;	Pred. NO. 1.5e-65;		
Matches 460;	Conservative 0;	Mismatches 26;	Indels 2;	Gaps 2;

Cy 1743 A^aA^bTGTTTCTATAGTCGGTGTAACTAATTACTTTTAATCAATAACATGTAAGAAGCGGTG 1802

Db 1 ACACTCTTTCTTCATAGTGGCTGTACACTCTTTCTTCATTTCTCCAACTCAACTGTGAAGCAAGGCTTTC 60

QY 1803 CCGTTCCTGACCACTCCCTCAGCACATTTATTATTGTGAACACTTCCTTGATACTGCAAGCCCAATTC 1962

Db 61 CCTTTTCCACACCCCTCTCCAGCATTATTCGTTGAGACITTTGGATAGCAGTCATTC 120

QY 1863 TCACTGCTGTGAATGGTACCTATACGCG-TTTGATTTGCATTCTTCGATAATGACTG 1921

D6 121 TCACTGGCGTGAATGTAACCCATCATTCGCGTTTGATTTCGATTTCTGTGATAACCAAGTG 180

Dh
181 ATCTGACCAATTTTGTATGTTCATTAGCCAAACTTAATGGTGCTCCTTAGAACAAAATCG 240

OY
1922 AATAAAGAATCATCTGAATGAGTGCATGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1981

QY 1982 TATTAGTCTTGGCCCA-TTTTGTATGGCTGTTATTTTCTGGAGTTCAGCTCT 2040

Db 241 TGTATTAGTTTTTGGGCGAGTTTTTGATTTGGGCTGTATTATTTCTGATATTTGAACTTAC 300

QY 2041 AGAGTTGCTGATATTTTGAGATTAGTGTTCGCGGTGCTTCATTGCTATTATT 2100

301 AGGAGTTGCTGTATATTTTGGAGTAATTTTGTGAGTTGCTCATTTGTAAT 360

2101 TTCTCCATTCTGAGGCTGTCTTTTCACCTTCTAATCATTTCTTTCATCTCTACAG 2160

361 TTTCTCCGATTTCTGAAGGCTATCTTTTCACTTCGTTTAAAGTTCCTCTGTTGTCGACGAAG 420

[illegible]

De 421 CCGTAAATTTAATAGAGCCCAATTTGTTATTTTGGCTTTATTTCCATATTTCCAAATATTTCTGGAA 480

File	Access
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098	1
099	1
100	1

5
4
3
2
1
0

RESULT 11
H1E80692/C

180705	494 BP	MBNA	150047	EST 17-SEP-2007
16160067				
459026	MARC 1BOV B05	tactus cDNA 5', mRNA sequence.		
DEFINITION				

ACCESSION	BI680692
VERSION	BI680692.1
GI	GI:15633606

ORGANISM	Doc	STATUS
SOURCE	COM.	EST.
KEYWORDS		

CORONARIUM
pos. caudus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

REFERENCE
1 (bases 1 to 484)
Bovidae; Bovinae; Bos.

AUTHORS Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, E., Wray, J. E., White, J., Cho, J., Palenikrug, S. C., Hemmelt

G. L., Heaton, M. P., Laegreid, W. W., Kohrer, G. A., Chitko-McKown, C. G.,
Perlea, G., Holt, I., Karanicheva, S., Liang, F., Quackenbush, J. and
Voigt, B.

TITLE Sequence evaluation of four pooled tissue normalized bovine CDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)
JOURNAL MEDLINE 21180013

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center

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